

SEQUENCE LISTING

<110> WANG, HUA
LUO, HONGLIANG
CONNOR, CHRIS
SCHWARTZ, STEVEN
YOUSEF, AHMED
WAN, KAI

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<141> 2003-12-02

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19

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18

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21

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<221> modified_base
<222> (666)..(666)
<223> a, c, g, or t

<220>
<221> modified_base
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<222> (679)..(679)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (715)..(715)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (975)..(975)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (1003)..(1003)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (1006)..(1006)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (1102)..(1102)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (1434)..(1434)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (1436)..(1436)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (1438)..(1438)
<223> a, c, g, or t

<400> 78
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gggccttcg gggccagcgg cggacgggtg agtaaacacgt gggtaatctg ctttcagac 120
cggaataacg cccggaaacg ggtgctaatg ccggatangc acgcgagnag gcatctnctt 180
gcggggaaag gtgcaantgc atcgctgaga gaggagcccg cggcgcatta gctagtttgt 240
ggggtaacgg ctcaccaagg cgacgatgcg tagccgacct gagagggtga ccggccacac 300
tgggactgag acacggccca gactcctacg ggaggcagca gtagggaatc ttccgcaatg 360
ggcgcaagcc tgacggagca acgcccgcgtg agcgaagaag gccttcgggt taaaagctc 420

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tgttgctcg	ggagagcggc	aaggggagt	gaaagccc	tgngagacgg	taccgagtga	480
ggaagccccg	gctaactacg	tgccagcagc	cgcgtaata	cgtggggc	aagcgttgc	540
cggaatca	ctact	ggcgtaaaag	cgtcgtagg	cggttgngta	agtctggagt	600
ggctcaaccn	tggaaatgct	ttggaaactg	cntgacttga	gtgctggaga	ggcaagggg	660
attccncgtg	tagcggtgna	atgcgtagat	atgtggagga	ataccagtgg	cgaangcgcc	720
ttgctggaca	gtgactgacg	ctgaggcacg	aaagcgtgg	gagcaaacag	gattagatac	780
cctggtagtc	cacgcccgtaa	acgatgagt	ctaggtgtt	gggggacaca	ccccagtgcc	840
gaaggaaacc	caataagcac	tccgcctgg	gagtacggc	gcaagactga	aactcaaagg	900
aattgacggg	ggcccgacaca	agcagtggag	catgtggttt	aattcgaagc	aacgcgaaga	960
accttaccag	ggctngacat	ccctctgaca	gccgcagaga	tgngnntcc	cttcggggca	1020
gaggagacag	gtggcgtcat	gttgcgtca	gctcggtcg	tgagatgtt	ggttaagtcc	1080
cgcaacgagc	gcaaccctt	gac	anctgtgtt	ccagcacgtt	gaggtgggg	1140
actgcccggcg	taagtcggag	gaaggcgggg	atgacgtcaa	atcatcatgc	cctttatgtc	1200
ctgggctaca	cacgtgctac	aatggcgggt	acaacgggaa	gcgaagccgc	gaggtggagc	1260
aaaacccaaa	aagccgttc	tagtcggat	tgcaggctc	aactcgcct	catgaagccg	1320
gaattgctag	taatcgccg	tcagcatgcc	gcggtaatc	cgttcccg	ccttgcac	1380
accgccccgtc	acaccacgag	agtcggcaac	acccgaagtc	ggtgaggtaa	cccnntnngg	1440
gagccagccg	ccgaagggtgg	ggttgcgtat	tgggtgaag	tcgtaacaag	gtagccgt	1498

<210> 79

<211> 718

<212> DNA

<213> *Alicyclobacillus acidocaldarius*

<400> 79

gggggttgg	tgttacaggc	ttccatctcg	cccggtgtgg	acacgggtct	cgccgtgc	60
gcgctgcgc	ctgcggggct	tccggccgat	cactgaccgg	ttggtaagg	ctgggctgaa	120
tggctgttgg	accggcagat	caccgtgc	ggcgattgg	ttgtgaagcg	cccgaaacctc	180
aacccgggcg	gcttcgcgt	ccagttcgac	aacgtgtact	atccggacgt	ggacgacacg	240
gccgtcgta	tctgggcgt	caacacgctg	cgactccgg	acgagcgc	caggcgagac	300
gccatgacga	agggattccg	gccatgacga	agggattccg	ctggattgtc	ggcatgcaga	360
gtcgaaacgg	cggtggggc	gcatacgacg	tcgacaacac	gagcgatctc	ccgaaccaca	420
tcccggtctg	cgacttcggc	gaagtgaccg	atccggccgtc	ggaagacgtc	accgcccacg	480
tgctcgatgt	tttcggcagc	tccggtac	acgacgcctg	gaaggtgtac	cagcgcgccg	540
tggcgtaac	caagcgggag	cagaagccgg	acggcagctg	gttcggtc	tggggcg	600
actacgtgt	tggcatcg	gcgggtgtgt	ccgcgtgaa	ggcggtcg	atcgacatgc	660
gcgagccgt	cattcaaaag	gcgctcgatt	gggtggagca	gcatcagaac	ccggacgg	718

<210> 80
 <211> 878
 <212> DNA
 <213> Alicyclobacillus acidocaldarius

<400> 80
 ggaggatgga tggccatctcg ccgggtgtggg acacgggcct cgccgtgctc 60
 gcgctgcgct ctgcggggct tccggccat cacgaccgct tggtaaggc gggcgagtgg 120
 ctgttggacc ggcagatcac ggttccggc gactggggc tgaagcgc 180
 ccgggcgggt tcgcgttcca gttcgacaac gtgtactacc cggacgtgga cgacacggcc 240
 gtcgtgggtt gggcgctcaa caccctgcgc ttgcggacg agcggccgag gcgacacggcc 300
 atgacgaagg gattccgctg gattgtcgac atgcagacgct cgaacggccg ttggggcgcc 360
 tacgacgtcg acaacacgag cgatctcccg aaccacatcc cgttctgcga cttcgccgaa 420
 gtgaccgatc cgccgtcaga ggacgtcacc gcccacgtgc tcgagtgaaa 480
 gggtaacatggaa ggtcatccgg cgcgcgggg aatatctcaa gcgacacggcc 540
 aagccggacg gcaatgggtt cggtcgttgg ggcgtcaattt acctctacgg cacggccg 600
 gtgggtgtgg cgctgaaggc ggtcggttgc gacacgcgcg agccgtatcat taaaaggcg 660
 ctcgactggg tcgagcagca tcagaaccccg gacggccggtt gggcgagga ctgcccgtcg 720
 tacgaggatc cggcgtaacgc gggtaaggc gcgagcaccc cgtcgacac ggcctgggg 780
 ctgatggcgc tcatcgccgg cggcaggccg gagtccgagg ccgcgcgcg cggcgtgcaa 840
 tacctcgatgg agacgcagcg cccggacggc ggctggga 878

<210> 81
 <211> 878
 <212> DNA
 <213> Alicyclobacillus acidoterrestris

<400> 81
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 gcactgcgtt cggctggattt gccaccatcatccagcgc tgattaaagc gggtgagtgg 120
 ttggtcagta aacaaatttca caaggatggc gactggaaag ttgcgtcgacg caaggcgaaa 180
 ccaggcggtt gggcatttga attccactgc gaaaactacc cagacgtcga cgatacggcc 240
 atggtcgttctt tggcgctcaa tggcattcaa ttgcggatg aaggaaagcg tcgtgacgca 300
 ttgaccctgtt gttccgttgc gttgcgcgatg atgcagatc cgaacggggg ctggggcgca 360
 tacatgtgg acaacacgcg tcagttgacc aatcgatcc cattttgcaat cttcgccgaa 420
 gtgattgatc cgccatcgaa agacgtcacc gcacacgtt tggatgtctt cggcagctt 480
 gggtaacatggaa ggtcatggaa ggtcatggc aaggcggtcg agtataatccaa ggcccaacaa 540
 cggccatcgatg ggtcatgggtt tggccgttgc ggcgtcaact acgtgtatgg catcgccg 600
 gtcgttccgg gactcaaggc cgtcggtgtc gatatgcgtg agccgtgggt gcaaaagtcg 660
 ctcgactggc tcgtcgagca taaaatgag gatggccggtt ggggtgaaag ccgaattcca 720
 gcacactggc ggccgttact agtggatccg agctcggtac caagcttggc gtaatcatgg 780
 tcatacgatgtt ttcctgtgtt aaattgttat ccgttcacaa ttcacacaac atacgagccg 840
 gaaacataatgtt gtaaggctgg ggtgcctatg agtggatctt 878

<210> 82
 <211> 878
 <212> DNA
 <213> Alicyclobacillus acidocaldarius

<400> 82
 ggggggttggga tggccatctcg ggttatttctt ccaatctggg atactggctt gaccgtcttg 60
 gcactgcgtt cggctggattt gccaccatcatccagcgc tgattaaagc gggtgagtgg 120
 ttggtcagta aacaaatttca caaggatggc gactggaaag ttgcgtcgacg caaggcgaaa 180
 ccaggcggtt gggcatttga attccactgc gaaaactacc cagacgtcga cgatacggcc 240

atggtcgtct tggcgctcaa tggcattcaa ttgccggatg aaggaaagcg tcgtgacgca 300
 ttgacccgtg gcttccgtg gttgcgcag atgcagagtt cgaacggggg ctggggcgca 360
 tacatgtgg acaacacgcg tcagttgacc aaatcgatt ccattttgc gacttcggc 420
 gaagtgattg atccgcccattc ggaagacgtc accgcacacg tcttggagtg cttcggcagc 480
 tttgggtacg acgaggcatg gaaggtgatt cgcaaggcgg tcgagtatct caaggcgc 540
 caacgcccag atgggtcatg gtttggccgc tggggcgta actacgtgta tggcatcg 600
 gcggtcgttc cgggactcaa ggccgtcggt gtcgatatgc gtgagccgtg ggtgcaaaag 660
 tcgctcgact ggctcgtcga gcatcaaaat gaggatggcg gttggggtga agattgcgt 720
 tcctatgtg atccacgtct cgcaggtcag ggtgtgagta caccgtcgca gaccgcctgg 780
 gcgttgcattgg cgctcatcgc gggccggcgt gtcgagtcag atgcggattt ggcgcggggtc 840
 acttaccttc acgacacgcg cgcgcagat ggtggctg 878

<210> 83

<211> 631

<212> PRT

<213> Alicyclobacillus acidocaldarius

<400> 83

Met	Ala	Glu	Gln	Leu	Val	Glu	Ala	Pro	Ala	Tyr	Ala	Arg	Thr	Leu	Asp
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Arg	Ala	Val	Glu	Tyr	Leu	Leu	Ser	Cys	Gln	Lys	Asp	Glu	Gly	Tyr	Trp
															30
20								25							

Trp	Gly	Pro	Leu	Leu	Ser	Asn	Val	Thr	Met	Glu	Ala	Glu	Tyr	Val	Leu
															45
35							40								

Leu	Cys	His	Ile	Leu	Asp	Arg	Val	Asp	Arg	Asp	Arg	Met	Glu	Lys	Ile
															60
50							55								

Arg	Arg	Tyr	Leu	Leu	His	Glu	Gln	Arg	Glu	Asp	Gly	Thr	Trp	Ala	Leu
															80
65					70			75							

Tyr	Pro	Gly	Gly	Pro	Pro	Asp	Leu	Asp	Thr	Thr	Ile	Glu	Ala	Tyr	Val
															95
85							90								

Ala	Leu	Lys	Tyr	Ile	Gly	Met	Ser	Arg	Asp	Glu	Glu	Pro	Met	Gln	Lys
															110
100							105								

Ala	Leu	Arg	Phe	Ile	Gln	Ser	Gln	Gly	Gly	Ile	Glu	Ser	Ser	Arg	Val
															125
115							120								

Phe	Thr	Arg	Met	Trp	Leu	Ala	Leu	Val	Gly	Glu	Tyr	Pro	Trp	Glu	Lys
															140
130							135								

Val	Pro	Met	Val	Pro	Pro	Glu	Ile	Met	Phe	Leu	Gly	Lys	Arg	Met	Pro
															160
145							150			155					

Leu	Asn	Ile	Tyr	Glu	Phe	Gly	Ser	Trp	Ala	Arg	Ala	Thr	Val	Val	Ala
															175
165								170							

Leu	Ser	Ile	Val	Met	Ser	Arg	Gln	Pro	Val	Phe	Pro	Leu	Pro	Glu	Arg
															190
180								185							

Ala	Arg	Val	Pro	Glu	Leu	Tyr	Glu	Thr	Asp	Val	Pro	Pro	Arg	Arg	Arg
															205
195								200							

Gly Ala Lys Gly Gly Gly Trp Ile Phe Asp Ala Leu Asp Arg Ala
 210 215 220

Leu His Gly Tyr Gln Lys Leu Ser Val His Pro Phe Arg Arg Ala Ala
 225 230 235 240

Glu Ile Arg Ala Leu Asp Trp Leu Leu Glu Arg Gln Ala Gly Asp Gly
 245 250 255

Ser Trp Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu
 260 265 270

Lys Ile Leu Asp Met Thr Gln His Pro Ala Phe Ile Lys Gly Trp Glu
 275 280 285

Gly Leu Glu Leu Tyr Gly Val Glu Leu Asp Tyr Gly Gly Trp Met Phe
 290 295 300

Gln Ala Ser Ile Ser Pro Val Trp Asp Thr Gly Leu Ala Val Leu Ala
 305 310 315 320

Leu Arg Ala Ala Gly Leu Pro Ala Asp His Asp Arg Leu Val Lys Ala
 325 330 335

Gly Glu Trp Leu Leu Asp Arg Gln Ile Thr Val Pro Gly Asp Trp Ala
 340 345 350

Val Lys Arg Pro Asn Leu Lys Pro Gly Gly Phe Ala Phe Gln Phe Asp
 355 360 365

Asn Val Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Val Trp Ala
 370 375 380

Leu Asn Thr Leu Arg Leu Pro Asp Glu Arg Arg Arg Arg Asp Ala Met
 385 390 395 400

Thr Lys Gly Phe Arg Trp Ile Val Gly Met Gln Ser Ser Asn Gly Gly
 405 410 415

Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser Asp Leu Pro Asn His Ile
 420 425 430

Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
 435 440 445

Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
 450 455 460

Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Lys
 465 470 475 480

Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
 485 490 495

Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Ile Asp Thr Arg
 500 505 510

Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
 515 520 525

Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
 530 535 540

Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
 545 550 555 560

Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Glu Ala Ala Arg Arg
 565 570 575

Gly Val Gln Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
 580 585 590

Glu Pro Tyr Tyr Thr Gly Thr Ala Ser Pro Gly Asp Phe Tyr Leu Gly
 595 600 605

Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
 610 615 620

Lys Gln Ala Ile Glu Arg Arg
 625 630

<210> 84
 <211> 631
 <212> PRT
 <213> Alicyclobacillus acidocaldarius

<400> 84
 Met Ala Glu Gln Leu Val Glu Ala Pro Ala Tyr Ala Arg Thr Leu Asp
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Arg Ala Val Glu Tyr Leu Leu Ser Cys Gln Lys Asp Glu Gly Tyr Trp
 20 25 30

Trp Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu
 35 40 45

Leu Cys His Ile Leu Asp Arg Val Asp Arg Asp Arg Met Glu Lys Ile
 50 55 60

Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Thr Trp Ala Leu
 65 70 75 80

Tyr Pro Gly Gly Pro Pro Asp Leu Asp Thr Thr Ile Glu Ala Tyr Val
 85 90 95

Ala Leu Lys Tyr Ile Gly Met Ser Arg Asp Glu Glu Pro Met Gln Lys
 100 105 110

Ala Leu Arg Phe Ile Gln Ser Gln Gly Gly Ile Glu Ser Ser Arg Val
 115 120 125

Phe Thr Arg Met Trp Leu Ala Leu Val Gly Glu Tyr Pro Trp Glu Lys
 130 135 140

Val Pro Met Val Pro Pro Glu Ile Met Phe Leu Gly Lys Arg Met Pro
 145 150 155 160

Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr Val Val Ala
 165 170 175

Leu Ser Ile Val Met Ser Arg Gln Pro Val Phe Pro Leu Pro Glu Arg
 180 185 190

Ala Arg Val Pro Glu Leu Tyr Glu Thr Asp Val Pro Pro Arg Arg Arg
 195 200 205

Gly Ala Lys Gly Gly Gly Trp Ile Phe Asp Ala Leu Asp Arg Ala
 210 215 220

Leu His Gly Tyr Gln Lys Leu Ser Val His Pro Phe Arg Arg Ala Ala
 225 230 235 240

Glu Ile Arg Ala Leu Asp Trp Leu Leu Glu Arg Gln Ala Gly Asp Gly
 245 250 255

Ser Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu
 260 265 270

Lys Ile Leu Asp Met Thr Gln His Pro Ala Phe Ile Lys Gly Trp Glu
 275 280 285

Gly Leu Glu Leu Tyr Gly Val Glu Leu Asp Tyr Gly Gly Trp Met Phe
 290 295 300

Gln Ala Ser Ile Ser Pro Val Trp Asp Thr Gly Leu Ala Val Leu Ala
 305 310 315 320

Leu Arg Ala Ala Gly Leu Pro Ala Asp His Asp Arg Leu Val Lys Ala
 325 330 335

Gly Glu Trp Leu Leu Asp Arg Gln Ile Thr Val Pro Gly Asp Trp Ala
 340 345 350

Val Lys Arg Pro Asn Leu Lys Pro Gly Gly Phe Ala Phe Gln Phe Asp
 355 360 365

Asn Val Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Val Trp Ala
 370 375 380

Leu Asn Thr Leu Arg Leu Pro Asp Glu Arg Arg Arg Asp Ala Met
 385 390 395 400

Thr Lys Gly Phe Arg Trp Ile Val Gly Met Gln Ser Ser Asn Gly Gly
 405 410 415

Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser Asp Leu Pro Asn His Ile
 420 425 430

Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
 435 440 445
 Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
 450 455 460
 Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Lys
 465 470 475 480
 Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
 485 490 495
 Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Ile Asp Thr Arg
 500 505 510
 Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
 515 520 525
 Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
 530 535 540
 Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
 545 550 555 560
 Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Glu Ala Ala Arg Arg
 565 570 575
 Gly Val Gln Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
 580 585 590
 Glu Pro Tyr Tyr Thr Gly Thr Gly Phe Pro Gly Asp Phe Tyr Leu Gly
 595 600 605
 Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
 610 615 620
 Lys Gln Ala Ile Glu Arg Arg
 625 630

<210> 85
 <211> 634
 <212> PRT
 <213> Alicyclobacillus acidoterrestris

<400> 85
 Met Thr Lys Gln Leu Leu Asp Thr Pro Met Val Gln Ala Thr Leu Glu
 1 5 10 15

Ala Gly Val Ala His Leu Leu Arg Arg Gln Ala Pro Asp Gly Tyr Trp
 20 25 30

Trp Ala Pro Leu Leu Ser Asn Val Cys Met Glu Ala Glu Tyr Val Leu
 35 40 45

Leu Cys His Cys Leu Gly Lys Lys Asn Pro Glu Arg Glu Ala Gln Ile
 50 55 60

Arg Lys Tyr Ile Ile Ser Gln Arg Arg Glu Asp Gly Thr Trp Ser Ile
 65 70 75 80

Tyr Pro Gly Gly Pro Ser Asp Leu Asn Ala Thr Val Glu Ala Tyr Val
 85 90 95

Ala Leu Lys Tyr Leu Gly Glu Pro Ala Ser Asp Pro Gln Met Val Gln
 100 105 110

Ala Lys Glu Phe Ile Gln Asn Glu Gly Gly Ile Glu Ser Thr Arg Val
 115 120 125

Phe Thr Arg Leu Trp Leu Ala Met Val Gly Gln Tyr Pro Trp Asp Lys
 130 135 140

Leu Pro Val Ile Pro Pro Glu Ile Met His Leu Pro Lys Ser Val Pro
 145 150 155 160

Leu Asn Ile Tyr Asp Phe Ala Ser Trp Ala Arg Ala Thr Ile Val Thr
 165 170 175

Leu Ser Tyr Arg His Glu Ser Pro Thr Cys Asp Ala Thr Ser Gly Leu
 180 185 190

Cys Lys Gly Ser Gly Ile Val Arg Gly Glu Gly Pro Pro Lys Arg Arg
 195 200 205

Ser Ala Lys Gly Gly Asp Ser Gly Phe Phe Val Ala Leu Asp Lys Phe
 210 215 220

Leu Lys Ala Tyr Asn Lys Trp Pro Ile Gln Pro Gly Arg Lys Ser Gly
 225 230 235 240

Glu Gln Lys Ala Leu Glu Trp Ile Leu Ala His Gln Glu Ala Asp Gly
 245 250 255

Cys Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Leu Ala Leu
 260 265 270

Lys Cys Leu Asn Met Thr Asp His Pro Ala Phe Val Lys Gly Phe Glu
 275 280 285

Gly Leu Glu Ala Tyr Gly Val His Thr Ser Asp Gly Gly Trp Met Phe
 290 295 300

Gln Ala Ser Ile Ser Pro Ile Trp Asp Thr Gly Leu Thr Val Leu Ala
 305 310 315 320

Leu Arg Ser Ala Gly Leu Pro Pro Asp His Pro Ala Leu Ile Lys Ala
 325 330 335

Gly Glu Trp Leu Val Ser Lys Gln Ile Leu Lys Asp Gly Asp Trp Lys
 340 345 350

Val Arg Arg Arg Lys Ala Lys Pro Gly Gly Trp Ala Phe Glu Phe His
 355 360 365

Cys Glu Asn Tyr Pro Asp Val Asp Asp Thr Ala Met Val Val Leu Ala
 370 375 380

Leu Asn Gly Ile Gln Leu Pro Asp Glu Gly Lys Arg Arg Asp Ala Leu
 385 390 395 400

Thr Arg Gly Phe Arg Trp Leu Arg Glu Met Gln Ser Ser Asn Gly Gly
 405 410 415

Trp Gly Ala Tyr Asp Val Asp Asn Thr Arg Gln Leu Thr Lys Ser Asp
 420 425 430

Ser Ile Phe Ala Thr Ser Gly Glu Val Ile Asp Pro Pro Ser Glu Asp
 435 440 445

Val Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Glu
 450 455 460

Ala Trp Lys Val Ile Arg Lys Ala Val Glu Tyr Leu Lys Ala Gln Gln
 465 470 475 480

Arg Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Val Tyr
 485 490 495

Gly Ile Gly Ala Val Val Pro Gly Leu Lys Ala Val Gly Val Asp Met
 500 505 510

Arg Glu Pro Trp Val Gln Lys Ser Leu Asp Trp Leu Val Glu His Gln
 515 520 525

Asn Glu Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Asp Asp Pro
 530 535 540

Arg Leu Ala Gly Gln Gly Val Ser Thr Pro Ser Gln Thr Ala Trp Ala
 545 550 555 560

Leu Met Ala Leu Ile Ala Gly Gly Arg Val Glu Ser Asp Ala Val Leu
 565 570 575

Arg Gly Val Thr Tyr Leu His Asp Thr Gln Arg Ala Asp Gly Gly Trp
 580 585 590

Asp Glu Glu Val Tyr Thr Gly Thr Gly Phe Pro Gly Asp Phe Tyr Leu
 595 600 605

Ala Tyr Thr Met Tyr Arg Asp Ile Leu Pro Val Trp Ala Leu Gly Arg
 610 615 620

Tyr Gln Glu Ala Met Gln Arg Ile Arg Gly
 625 630

<210> 86
 <211> 556
 <212> PRT
 <213> *Bacillus subtilis*

<400> 86
 Met Gly Thr Leu Gln Glu Lys Val Arg Arg Phe Gln Lys Lys Thr Ile
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 Thr Glu Leu Arg Asp Arg Gln Asn Ala Asp Gly Ser Trp Thr Phe Cys
 20 25 30
 Phe Glu Gly Pro Ile Met Thr Asn Ser Phe Phe Ile Leu Leu Leu Thr
 35 40 45
 Ser Leu Asp Glu Gly Glu Asn Glu Lys Glu Leu Ile Ser Ser Leu Ala
 50 55 60
 Ala Gly Ile His Ala Lys Gln Gln Pro Asp Gly Thr Phe Ile Asn Tyr
 65 70 75 80
 Pro Asp Glu Thr Arg Gly Asn Leu Thr Ala Thr Val Gln Gly Tyr Val
 85 90 95
 Gly Met Leu Ala Ser Gly Cys Phe His Arg Thr Glu Pro His Met Lys
 100 105 110
 Lys Ala Glu Gln Phe Ile Ile Ser His Gly Gly Leu Arg His Val His
 115 120 125
 Phe Met Thr Lys Trp Met Leu Ala Ala Asn Gly Leu Tyr Pro Trp Pro
 130 135 140
 Ala Leu Tyr Leu Pro Leu Ser Leu Met Ala Leu Pro Pro Thr Leu Pro
 145 150 155 160
 Ile His Phe Tyr Gln Phe Ser Ser Tyr Ala Arg Ile His Phe Ala Pro
 165 170 175
 Met Ala Val Thr Leu Asn Gln Arg Phe Val Leu Ile Asn Arg Asn Ile
 180 185 190
 Ser Ser Leu His His Leu Asp Pro His Met Thr Lys Asn Pro Phe Thr
 195 200 205
 Trp Leu Arg Ser Asp Ala Phe Glu Glu Arg Asp Leu Thr Ser Ile Leu
 210 215 220
 Leu His Trp Lys Arg Val Phe His Ala Pro Phe Ala Phe Gln Gln Leu
 225 230 235 240
 Gly Leu Gln Thr Ala Lys Thr Tyr Met Leu Asp Arg Ile Glu Lys Asp
 245 250 255
 Gly Thr Leu Tyr Ser Tyr Ala Ser Ala Thr Ile Tyr Met Val Tyr Ser
 260 265 270
 Leu Leu Ser Leu Gly Val Ser Arg Tyr Ser Pro Ile Ile Arg Arg Ala
 275 280 285

Ile Thr Gly Ile Lys Ser Leu Val Thr Lys Cys Asn Gly Ile Pro Tyr
 290 295 300
 Leu Glu Asn Ser Thr Ser Thr Val Trp Asp Thr Ala Leu Ile Ser Tyr
 305 310 315 320
 Ala Leu Gln Lys Asn Gly Val Thr Glu Thr Asp Gly Ser Val Thr Lys
 325 330 335
 Ala Ala Asp Phe Leu Leu Glu Arg Gln His Thr Lys Ile Ala Asp Trp
 340 345 350
 Ser Val Lys Asn Pro Asn Ser Val Pro Gly Gly Trp Gly Phe Ser Asn
 355 360 365
 Ile Asn Thr Asn Asn Pro Asp Cys Asp Asp Thr Thr Ala Val Leu Lys
 370 375 380
 Ala Ile Pro Arg Asn His Ser Pro Ala Ala Trp Glu Arg Gly Val Ser
 385 390 395 400
 Trp Leu Leu Ser Met Gln Asn Asn Asp Gly Gly Phe Ser Ala Phe Glu
 405 410 415
 Lys Asn Val Asn His Pro Leu Ile Arg Leu Leu Pro Leu Glu Ser Ala
 420 425 430
 Glu Asp Ala Ala Val Asp Pro Ser Thr Ala Asp Leu Thr Gly Arg Val
 435 440 445
 Leu His Phe Leu Gly Glu Lys Val Gly Phe Thr Glu Lys His Gln His
 450 455 460
 Ile Gln Arg Ala Val Lys Trp Leu Phe Glu His Gln Glu Gln Asn Gly
 465 470 475 480
 Ser Trp Tyr Gly Arg Trp Gly Val Cys Tyr Ile Tyr Gly Thr Trp Ala
 485 490 495
 Ala Leu Thr Gly Met His Ala Cys Gly Leu Thr Glu Ser Ile Pro Val
 500 505 510
 Tyr Lys Arg Leu Cys Val Gly Ser Asn Pro Tyr Lys Met Met Thr Glu
 515 520 525
 Ala Gly Glu Asn Pro Ala Lys Ala Pro Lys Ser Lys His Met Tyr Arg
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 Phe Ile Glu Glu Pro Leu Tyr Lys Arg Pro Gly Leu
 545 550 555

<210> 87
 <211> 706

<212> PRT

<213> Dictyostelium discoideum

<400> 87

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Arg Gln Thr Trp Glu Tyr Ser Gln Glu Lys Lys Glu Ala Thr Asp Val																	
				20					25					30			
Asp Ile His Leu Leu Arg Leu Lys Glu Pro Gly Thr His Cys Pro Glu																	
				35					40					45			
Gly Cys Asp Leu Asn Arg Ala Lys Thr Pro Gln Gln Ala Ile Lys Lys																	
				50					55					60			
Ala Phe Gln Tyr Phe Ser Lys Val Gln Thr Glu Asp Gly His Trp Ala																	
				65					70					75			80
Gly Asp Tyr Gly Gly Pro Met Phe Leu Leu Pro Gly Leu Val Ile Thr																	
				85					90					95			
Cys Tyr Val Thr Gly Tyr Gln Leu Pro Glu Ser Thr Gln Arg Glu Ile																	
				100					105					110			
Ile Arg Tyr Leu Phe Asn Arg Gln Asn Pro Val Asp Gly Gly Trp Gly																	
				115					120					125			
Leu His Ile Glu Ala His Ser Asp Ile Phe Gly Thr Thr Leu Gln Tyr																	
				130					135					140			
Val Ser Leu Arg Leu Leu Gly Val Pro Ala Asp His Pro Ser Val Val																	
				145					150					155			160
Lys Ala Arg Thr Phe Leu Leu Gln Asn Gly Gly Ala Thr Gly Ile Pro																	
				165					170					175			
Ser Trp Gly Lys Phe Trp Leu Ala Thr Leu Asn Ala Tyr Asp Trp Asn																	
				180					185					190			
Gly Leu Asn Pro Ile Pro Ile Glu Phe Trp Leu Leu Pro Tyr Asn Leu																	
				195					200					205			
Pro Ile Ala Pro Gly Arg Trp Trp Cys His Cys Arg Met Val Tyr Leu																	
				210					215					220			
Pro Met Ser Tyr Ile Tyr Ala Lys Lys Thr Thr Gly Pro Leu Thr Asp																	
				225					230					235			240
Leu Val Lys Asp Leu Arg Arg Glu Ile Tyr Cys Gln Glu Tyr Glu Lys																	
				245					250					255			
Ile Asn Trp Ser Glu Gln Arg Asn Asn Ile Ser Lys Leu Asp Met Tyr																	
				260					265					270			
Tyr Glu His Thr Ser Leu Leu Asn Val Ile Asn Gly Ser Leu Asn Ala																	
				275					280					285			

Tyr Glu Lys Val His Ser Lys Trp Leu Arg Asp Lys Ala Ile Asp Tyr
 290 295 300

Thr Phe Asp His Ile Arg Tyr Glu Asp Glu Gln Thr Lys Tyr Ile Asp
 305 310 315 320

Ile Gly Pro Val Asn Lys Thr Val Asn Met Leu Cys Val Trp Asp Arg
 325 330 335

Glu Gly Lys Ser Pro Ala Phe Tyr Lys His Ala Asp Arg Leu Lys Asp
 340 345 350

Tyr Leu Trp Leu Ser Phe Asp Gly Met Lys Met Gln Gly Tyr Asn Gly
 355 360 365

Ser Gln Leu Trp Asp Thr Ala Phe Thr Ile Gln Ala Phe Met Glu Ser
 370 375 380

Gly Ile Ala Asn Gln Phe Gln Asp Cys Met Lys Leu Ala Gly His Tyr
 385 390 395 400

Leu Asp Ile Ser Gln Val Pro Glu Asp Ala Arg Asp Met Lys His Tyr
 405 410 415

His Arg His Tyr Ser Lys Gly Ala Trp Pro Phe Ser Thr Val Asp His
 420 425 430

Gly Trp Pro Ile Ser Asp Cys Thr Ala Glu Gly Ile Lys Ser Ala Leu
 435 440 445

Ala Leu Arg Ser Leu Pro Phe Ile Glu Pro Ile Ser Leu Asp Arg Ile
 450 455 460

Ala Asp Gly Ile Asn Val Leu Leu Thr Leu Gln Asn Gly Asp Gly Gly
 465 470 475 480

Trp Ala Ser Tyr Glu Asn Thr Arg Gly Pro Lys Trp Leu Glu Lys Phe
 485 490 495

Asn Pro Ser Glu Val Phe Gln Asn Ile Met Ile Asp Tyr Ser Tyr Val
 500 505 510

Glu Cys Ser Ala Ala Cys Ile Gln Ala Met Ser Ala Phe Arg Lys His
 515 520 525

Ala Pro Asn His Pro Arg Ile Lys Glu Ile Asn Arg Ser Ile Ala Arg
 530 535 540

Gly Val Lys Phe Ile Lys Ser Ile Gln Arg Gln Asp Gly Ser Trp Leu
 545 550 555 560

Gly Ser Trp Gly Ile Cys Phe Thr Tyr Gly Thr Trp Phe Gly Ile Glu
 565 570 575

Gly Leu Val Ala Ser Gly Glu Pro Leu Thr Ser Pro Ser Ile Val Lys
 580 585 590

Ala Cys Lys Phe Leu Ala Ser Lys Gln Arg Ala Asp Gly Gly Trp Gly
 595 600 605

Glu Ser Phe Lys Ser Asn Val Thr Lys Glu Tyr Val Gln His Glu Thr
 610 615 620

Ser Gln Val Val Asn Thr Gly Trp Ala Leu Leu Ser Leu Met Ser Ala
 625 630 635 640

Lys Tyr Pro Asp Arg Glu Cys Ile Glu Arg Gly Ile Lys Phe Leu Ile
 645 650 655

Gln Arg Gln Tyr Pro Asn Gly Asp Phe Pro Gln Glu Ser Ile Ile Gly
 660 665 670

Val Phe Asn Phe Asn Cys Met Ile Ser Tyr Ser Asn Tyr Lys Asn Ile
 675 680 685

Phe Pro Leu Trp Ala Leu Ser Arg Tyr Asn Gln Leu Tyr Leu Lys Ser
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Lys Ile
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<210> 88
 <211> 647
 <212> PRT
 <213> Synechocystis PCC6803

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 35 40 45

Thr Ala Glu Val Val Ile Leu His Lys Ile Trp Gly Thr Ala Ala Gln
 50 55 60

Arg Pro Leu Glu Lys Ala Lys Asn Tyr Leu Leu Gln Gln Gln Arg Asp
 65 70 75 80

His Gly Gly Trp Glu Leu Tyr Tyr Gly Asp Gly Gly Glu Leu Ser Thr
 85 90 95

Ser Val Glu Ala Tyr Thr Ala Leu Arg Ile Leu Gly Val Pro Ala Thr
 100 105 110

Asp Pro Ala Leu Val Lys Ala Lys Asn Phe Ile Val Gly Arg Gly Gly
 115 120 125

Ile Ser Lys Ser Arg Ile Phe Thr Lys Met His Leu Ala Leu Ile Gly
 130 135 140

Cys Tyr Asp Trp Arg Gly Thr Pro Ser Ile Pro Pro Trp Val Met Leu
 145 150 155 160

Leu Pro Asn Asn Phe Phe Asn Ile Tyr Glu Met Ser Ser Trp Ala
 165 170 175

Arg Ser Ser Thr Val Pro Leu Met Ile Val Cys Asp Gln Lys Pro Val
 180 185 190

Tyr Asp Ile Ala Gln Gly Leu Arg Val Asp Glu Leu Tyr Ala Glu Gly
 195 200 205

Met Glu Asn Val Gln Tyr Lys Leu Pro Glu Ser Gly Thr Ile Trp Asp
 210 215 220

Ile Phe Ile Gly Leu Asp Ser Leu Phe Lys Leu Gln Glu Gln Ala Lys
 225 230 235 240

Val Val Pro Phe Arg Glu Gln Gly Leu Ala Leu Ala Glu Lys Trp Ile
 245 250 255

Leu Glu Arg Gln Glu Val Ser Gly Asp Trp Gly Gly Ile Ile Pro Ala
 260 265 270

Met Leu Asn Ser Leu Leu Ala Leu Lys Val Leu Gly Tyr Asp Val Asn
 275 280 285

Asp Leu Tyr Val Gln Arg Gly Leu Ala Ala Ile Asp Asn Phe Ala Val
 290 295 300

Glu Thr Glu Asp Ser Tyr Ala Ile Gln Ala Cys Val Ser Pro Val Trp
 305 310 315 320

Asp Thr Ala Trp Val Val Arg Ala Leu Ala Glu Ala Asp Leu Gly Lys
 325 330 335

Asp His Pro Ala Leu Val Lys Ala Gly Gln Trp Leu Leu Asp Lys Gln
 340 345 350

Ile Leu Thr Tyr Gly Asp Trp Gln Ile Lys Asn Pro His Gly Glu Pro
 355 360 365

Gly Ala Trp Ala Phe Glu Phe Asp Asn Asn Phe Tyr Pro Asp Ile Asp
 370 375 380

Asp Thr Cys Val Val Met Met Ala Leu Gln Gly Ile Thr Leu Pro Asp
 385 390 395 400

Glu Glu Arg Lys Gln Gly Ala Ile Asn Lys Ala Leu Gln Trp Ile Ala
 405 410 415

Thr Met Gln Cys Lys Thr Gly Gly Trp Ala Ala Phe Asp Ile Asp Asn
 420 425 430

Asp Gln Asp Trp Leu Asn Gln Leu Pro Tyr Gly Asp Leu Lys Ala Met
 435 440 445
 Ile Asp Pro Ser Thr Ala Asp Ile Thr Ala Arg Val Val Glu Met Leu
 450 455 460
 Gly Ala Cys Gly Leu Thr Met Asp Ser Pro Arg Val Glu Arg Gly Leu
 465 470 475 480
 Thr Tyr Leu Leu Gln Glu Gln Asp Gly Ser Trp Phe Gly Arg
 485 490 495
 Trp Gly Val Asn Tyr Leu Tyr Gly Thr Ser Gly Ala Leu Ser Ala Leu
 500 505 510
 Ala Ile Tyr Asp Ala Gln Arg Phe Ala Pro Gln Ile Lys Thr Ala Ile
 515 520 525
 Ala Trp Leu Leu Ser Cys Gln Asn Ala Asp Gly Gly Trp Gly Glu Thr
 530 535 540
 Cys Glu Ser Tyr Lys Asn Lys Gln Leu Lys Gly Gln Gly Asn Ser Thr
 545 550 555 560
 Ala Ser Gln Thr Ala Trp Ala Leu Ile Gly Leu Leu Asp Ala Leu Lys
 565 570 575
 Tyr Leu Pro Ser Leu Gly Gln Asp Ala Lys Leu Thr Thr Ala Ile Glu
 580 585 590
 Gly Gly Val Ala Phe Leu Val Gln Gly Gln Thr Pro Lys Gly Thr Trp
 595 600 605
 Glu Glu Ala Glu Tyr Thr Gly Thr Gly Phe Pro Cys His Phe Tyr Ile
 610 615 620
 Arg Tyr His Tyr Tyr Arg Gln Tyr Phe Pro Leu Ile Ala Leu Ala Arg
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 Tyr Ser His Leu Gln Ala Ser
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<210> 89
 <211> 680
 <212> PRT
 <213> Streptomyces coelicolor

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 Gly Val Pro Glu Ala Ala Ala Arg Ala Thr Arg Arg Ala Thr Asp Phe
 35 40 45

Leu Leu Ala Lys Gln Asp Ala Glu Gly Trp Trp Lys Gly Asp Leu Glu
 50 55 60

Thr Asn Val Thr Met Asp Ala Glu Asp Leu Leu Leu Arg Gln Phe Leu
 65 70 75 80

Gly Ile Gln Asp Glu Glu Thr Thr Arg Ala Ala Ala Leu Phe Ile Arg
 85 90 95

Gly Glu Gln Arg Glu Asp Gly Thr Trp Ala Thr Phe Tyr Gly Gly Pro
 100 105 110

Gly Glu Leu Ser Thr Thr Ile Glu Ala Tyr Val Ala Leu Arg Leu Ala
 115 120 125

Gly Asp Ser Pro Glu Ala Pro His Met Ala Arg Ala Ala Glu Trp Ile
 130 135 140

Arg Ser Arg Gly Gly Ile Ala Ser Ala Arg Val Phe Thr Arg Ile Trp
 145 150 155 160

Leu Ala Leu Phe Gly Trp Trp Lys Trp Asp Asp Leu Pro Glu Leu Pro
 165 170 175

Pro Glu Leu Ile Tyr Phe Pro Thr Trp Val Pro Leu Asn Ile Tyr Asp
 180 185 190

Phe Gly Cys Trp Ala Arg Gln Thr Ile Val Pro Leu Thr Ile Val Ser
 195 200 205

Ala Lys Arg Pro Val Arg Pro Ala Pro Phe Pro Leu Asp Glu Leu His
 210 215 220

Thr Asp Pro Ala Arg Pro Asn Pro Pro Arg Pro Leu Ala Pro Val Ala
 225 230 235 240

Ser Trp Asp Gly Ala Phe Gln Arg Ile Asp Lys Ala Leu His Ala Tyr
 245 250 255

Arg Lys Val Ala Pro Arg Arg Leu Arg Arg Ala Ala Met Asn Ser Ala
 260 265 270

Ala Arg Trp Ile Ile Glu Arg Gln Glu Asn Asp Gly Cys Trp Gly Gly
 275 280 285

Ile Gln Pro Pro Ala Val Tyr Ser Val Ile Ala Leu Tyr Leu Leu Gly
 290 295 300

Tyr Asp Leu Glu His Pro Val Met Arg Ala Gly Leu Glu Ser Leu Asp
 305 310 315 320

Arg Phe Ala Val Trp Arg Glu Asp Gly Ala Arg Met Ile Glu Ala Cys
 325 330 335

Gln Ser Pro Val Trp Asp Thr Cys Leu Ala Thr Ile Ala Leu Ala Asp
 340 345 350

Ala Gly Val Pro Glu Asp His Pro Gln Leu Val Lys Ala Ser Asp Trp
 355 360 365
 Met Leu Gly Glu Gln Ile Val Arg Pro Gly Asp Trp Ser Val Lys Arg
 370 375 380
 Pro Gly Leu Pro Pro Gly Gly Trp Ala Phe Glu Phe His Asn Asp Asn
 385 390 395 400
 Tyr Pro Asp Ile Asp Asp Thr Ala Glu Val Val Leu Ala Leu Arg Arg
 405 410 415
 Val Arg His His Asp Pro Glu Arg Val Glu Lys Ala Ile Gly Arg Gly
 420 425 430
 Val Arg Trp Asn Leu Gly Met Gln Ser Lys Asn Gly Ala Trp Gly Ala
 435 440 445
 Phe Asp Val Asp Asn Thr Ser Ala Phe Pro Asn Arg Leu Pro Phe Cys
 450 455 460
 Asp Phe Gly Glu Val Ile Asp Pro Pro Ser Ala Asp Val Thr Ala His
 465 470 475 480
 Val Val Glu Met Leu Ala Val Glu Gly Leu Ala His Asp Pro Arg Thr
 485 490 495
 Arg Arg Gly Ile Gln Trp Leu Leu Asp Ala Gln Glu Thr Asp Gly Ser
 500 505 510
 Trp Phe Gly Arg Trp Gly Val Asn Tyr Val Tyr Gly Thr Gly Ser Val
 515 520 525
 Ile Pro Ala Leu Thr Ala Ala Gly Leu Pro Thr Ser His Pro Ala Ile
 530 535 540
 Arg Arg Ala Val Arg Trp Leu Glu Ser Val Gln Asn Glu Asp Gly Gly
 545 550 555 560
 Trp Gly Glu Asp Leu Arg Ser Tyr Arg Tyr Val Arg Glu Trp Ser Gly
 565 570 575
 Arg Gly Ala Ser Thr Ala Ser Gln Thr Gly Trp Ala Leu Met Ala Leu
 580 585 590
 Leu Ala Ala Gly Glu Arg Asp Ser Lys Ala Val Glu Arg Gly Val Ala
 595 600 605
 Trp Leu Ala Ala Thr Gln Arg Glu Asp Gly Ser Trp Asp Glu Pro Tyr
 610 615 620
 Phe Thr Gly Thr Gly Phe Pro Trp Asp Phe Ser Ile Asn Tyr Asn Leu
 625 630 635 640
 Tyr Arg Gln Val Phe Pro Leu Thr Ala Leu Gly Arg Tyr Val His Gly
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Glu Pro Phe Ala Lys Lys Pro Arg Ala Ala Asp Ala Pro Ala Glu Ala
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Ala Pro Ala Glu Val Lys Gly Ser
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<210> 90
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majority sequence

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Xaa Xaa
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Xaa Xaa Xaa Xaa Xaa Xaa Glu Ala Val Ala Arg Ala Leu Asp Arg
50           55           60

Ala Val Asp Tyr Leu Leu Ser Arg Gln Lys Ala Asp Gly Tyr Trp Trp
65           70           75           80

Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu Leu
85           90           95

Cys His Ile Leu Gly Arg Val Asp Arg Glu Arg Xaa Xaa Met Glu Lys
100          105          110

Ile Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Thr Trp Ala
115          120          125

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Leu Tyr Pro Gly Gly Pro Xaa Gly Asp Leu Ser Thr Thr Val Glu Ala
 130 135 140

Tyr Val Ala Leu Lys Tyr Leu Gly Xaa Val Ser Ala Asp Glu Pro His
 145 150 155 160

Met Val Lys Ala Leu Glu Phe Ile Gln Ser Gln Gly Gly Ile Glu Ser
 165 170 175

Ser Arg Val Phe Thr Arg Met Trp Leu Ala Leu Val Gly Glu Tyr Pro
 180 185 190

Trp Asp Lys Leu Pro Met Ile Pro Pro Glu Ile Met Leu Leu Pro Lys
 195 200 205

Asn Val Pro Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr
 210 215 220

Val Val Pro Leu Ser Ile Val Met Ala Gln Gln Pro Val Xaa Xaa Xaa
 225 230 235 240

Xaa Phe Pro Leu Pro Glu Leu Ala Arg Val Pro Glu Leu Tyr Glu Thr
 245 250 255

Asp Val Pro Pro Arg Arg Xaa Arg Gly Ala Lys Gly Gly Gly Trp
 260 265 270

Xaa Xaa Xaa Ile Phe Asp Ala Xaa Xaa Leu Asp Ser Ala Leu His Gly
 275 280 285

Tyr Gln Lys Ala Xaa Xaa Ala Val His Pro Phe Arg Arg Ala Gly Glu
 290 295 300

Ala Arg Ala Leu Thr Trp Ile Leu Glu Arg Gln Glu Gly Asp Gly Ser
 305 310 315 320

Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu Lys
 325 330 335

Val Leu Gly Met Thr Xaa Gln His Pro Ala Phe Ile Lys Gly Leu Glu
 340 345 350

Gly Leu Glu Leu Tyr Gly Val Glu Leu Ser Asp Gly Gly Trp Met Phe
 355 360 365

Gln Ala Xaa Ser Ile Ser Pro Val Trp Asp Thr Gly Leu Ala Val Leu
 370 375 380

Ala Leu Arg Ala Ala Gly Leu Pro Ala Asp His Pro Ala Leu Val Lys
 385 390 395 400

Ala Gly Glu Trp Leu Leu Asp Arg Gln Ile Thr Val Pro Gly Asp Trp
 405 410 415

Ala Val Lys Arg Xaa Xaa Pro Asn Leu Lys Pro Gly Gly Trp Ala Phe
 420 425 430

Glu Phe Asp Asn Val Asn Tyr Pro Asp Val Asp Asp Thr Ala Val Val
 435 440 445

Val Xaa Xaa Xaa Leu Ala Leu Asn Gly Leu Arg Leu Pro Asp Glu Glu
 450 455 460

Arg Arg Arg Asp Ala Ile Thr Lys Gly Phe Arg Trp Leu Leu Gly Met
 465 470 475 480

Gln Ser Ser Asn Gly Gly Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser
 485 490 495

Asp Leu Pro Asn His Leu Pro Xaa Phe Cys Asp Phe Gly Glu Val Xaa
 500 505 510

Ile Asp Pro Pro Ser Ala Asp Val Thr Ala His Val Leu Glu Cys Leu
 515 520 525

Gly Ser Xaa Xaa Xaa Phe Gly Xaa Xaa Xaa Xaa Xaa Tyr Asp Glu Ala
 530 535 540

Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Glu
 545 550 555 560

Gln Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
 565 570 575

Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Leu Asp Thr Arg
 580 585 590

Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Leu Glu Ser His Gln Asn
 595 600 605

Ala Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Xaa Asp Pro
 610 615 620

Glu Tyr Ala Gly Gln Gly Ala Ser Thr Ala Ser Gln Thr Ala Trp Ala
 625 630 635 640

Leu Met Ala Leu Ile Ala Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Arg
 645 650 655

Ala Glu Xaa Xaa Ser Glu Ala Ala Glu Arg Gly Val Ala Tyr Leu Val
 660 665 670

Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp Glu Pro Tyr Tyr Thr Gly
 675 680 685

Thr Gly Phe Pro Gly Asp Phe Tyr Leu Gly Tyr Thr Met Tyr Arg Gln
 690 695 700

Val Phe Pro Leu Leu Ala Leu Gly Arg Tyr Lys Gln Ala Xaa Xaa Xaa
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Xaa
 725 730 735

Glu Arg Xaa Gly Ser
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<210> 91

<211> 376

<212> DNA

<213> Zygosaccharomyces bailii

<400> 91

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 tatcggttcc aagccgatgg aagtttgagg caataacagg tctgtatgc ccttagacgt 180
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 <213> *Penicillium chrysogenum*

<400> 98
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 gcccgtggct tcttaggggg actatcggctt caagccgtt gaaatgcgcg gcaataacag 180
 gtctgtgtatg cccttagatg ttctggccgc caccgcgcgtt acactgacag gggccagcgg 240
 tacatcacct taaccgagag gtttgggtt tcttgcgtt ccctgtcg tggctgggatag 300
 agcattgcaat tatttgcgtt tcaacgagg aatgcctagta ggcacgagtc atcagctgt 360
 gccgattacg tccctgccc ttgtacacac cggccgtcg tactaccgt tgaatg 416

<210> 99
 <211> 406
 <212> DNA
 <213> *Aspergillus nidulans*

<400> 99
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 cggggcgcgtg gcttcttagg gggactatcg gctcaagccg atgaaagtgc gcggcaataa 180
 caggtctgtg atgccttagt atgttctggg ccgcacgcgc gctacactga cagggccagc 240
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 cgtgccgatt acgtccctgc ccttgtaca caccgccccgt cgctac 406

<210> 100
 <211> 427
 <212> DNA
 <213> *Eurotium amstelodami*

<400> 100
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 cgctggcttc tttaggggac tatcgctca agccgatggg agtgcgcggc aataacaggt 180
 ctgtgatgcc ctttagatgtt ctggccgcga cgcgcgtac actgacaggg ccagcgagta 240
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 cattgcaatt attgcttc aacgaggaat gcctagtagg cacgagtcat cagctcgtgc 360
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 tgaggcc 427

<210> 101
 <211> 442
 <212> DNA
 <213> *Aspergillus candidus*

<400> 101
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 ggcgcgtggc ttcttagggg gactatcgcc tcaagccgat ggaagtgcgc ggcataaaca 180
 ggtctgtat gcccttagat gttctgggcgc gacacgcgcg tacactgaca gggccagcga 240
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 gagcattgca attattgtctt ttcacgagg aatgcctagt aggcacgagg catcagctcg 360
 tgccgatttttac gtccctgccc tttgtacaca cccgtcgctc ctactaccga ttgaatggct 420
 cggtgaggcc tccggactgg ct 442

<210> 102
 <211> 407
 <212> DNA
 <213> *Gallus gallus*

<400> 102
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 ctggtaattt ccgataacga acgagactct ggcattgttca ctagttacgc gaccccccgg 120
 cggtcggcgtt ccaacttctt agagggacaa gtggcggttca gccacccggat attgagcaat 180
 aacaggtctg tgatgccctt agatgtccgg ggctgcacgc ggcgtacact gactggctca 240
 gcttgggtctt accctacggcc ggcaggcgcc ggttaacccgt tgaacccat tcgtgatggg 300
 gatcggggat tgcaattttt ccccatgaac gaggaattcc cagtaagtgc gggtcataag 360
 ctcgcgttga ttaagtccctt gcccttggta cacaccgccccgt gtcgctca 407

<210> 103
 <211> 407

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<212> DNA
<213> Triticum aestivum

<400> 103
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ctcccgagct agcttcttag agggactatac gccgtttagg cgacggaagt ttgaggcaat 180
aacaggtctg tgatgccctt agatgttctg ggccgcacgc ggcgtacact gatgtattca 240
acgagtatat agccttggcc gacaggcccg ggtaatcttgg gaaatttca tcgtgatggg 300
gatacat tgcaattgtt ggtttcaac gaggaatgcc tagtaagcgc gagtcatcag 360
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<210> 104
<211> 411
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Figure 7
      consensus sequence

<220>
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<222> (96)..(96)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (106)..(106)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (115)..(116)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (118)..(119)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (131)..(131)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (158)..(158)
<223> a, c, g, or t

<400> 104
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tttgcgggcc ngctggcttc ttagagggac tatcggcntc aagccgatgg aagtttgcgg	180
caataacagg tctgtgatgc ccttagatgt tctgggcccgc acgcgcgcta cactgacggg	240
gccagcgagt acataaacctt ggccgagagg tctgggtaat cttgtgaaac cctgtcggtc	300
tggggataga gcattgcaat tattgctt caacgaggaa tgcctagtag gcgcgagtca	360
tcagctcgta ttgattacgt ccctgccc ttgtacacacc gcccgtcgct a	411
<210> 105	
<211> 19	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
oligonucleotide primer	
<400> 105	
gtggtgctag catttgctg	19
<210> 106	
<211> 17	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
oligonucleotide primer	
<400> 106	
ccgctggctt cttaggg	17
<210> 107	
<211> 18	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
oligonucleotide primer	
<400> 107	
ggagccagcg agtctaac	18
<210> 108	
<211> 19	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	

oligonucleotide primer

<400> 108
aggcccagcg agtacatca 19

<210> 109
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 109
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<210> 110
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 110
ctcaagccga tggaaagtgcg 20

<210> 111
<211> 1500
<212> DNA
<213> Alicyclobacillus acidocaldarius

<400> 111
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ttgcggggga aggcccaatt gggtcgctga gagaggagcc cgccggcgcat tagctagttg 240
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gaattccacg ttagcggtt aaatgcgttag agatgtggag gaataaccagt ggcgaargcg 720
ccttgcttggaa cagtgcgtt cgtgcgtt cggaaaggcgtt gggagcaaac aggatttagat 780
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 tcctgggcta cacacgtgt acaatggcgg gaacaaaggg aggccaagcc gcgaggcgg 1260
 gcaaaaccca aaaagccgt cgtatccgg attgcaggct gcaactcgcc tgcataa 1320
 cggaattgtc agtaatcgcg gatcagcatg ccgcgggtgaa tacgttcccg ggccttgc 1380
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<210> 112
 <211> 1520
 <212> DNA
 <213> *Alicyclobacillus acidocaldarius*

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 <222> (236)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (462)
 <223> a, t, c or g

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 gcccgaataa cggccggaaa cggcgctaa tgccgatac gcccgcgagg aggcata 180
 ttgcggggaa aggcccaatt gggccgtga gagaggagcc cgcggcgcat tagctngtt 240
 gcggggtaac ggcccaccaa ggcgacgtg ctagccgac ctgagagggt gaccggccac 300
 actgggactg agacacggcc cagactcta cgggaggcag cagtagggaa tcttccgca 360
 tggcgcaag cctgacggag caacgcccgg tgagcgaaga aggccctcg 420
 tctgttgc ggggagagcg gcatggggta tggaaagccc cngcgcgac ggtaccgagt 480
 gaggaagccc cggctacta cgtggccgca gcccggtaa aacgtgggg gcgagcgtt 540
 tccggaatca ctggggctaa agggtgcgtg ggcggcgtg caagtcgtt 600
 atggctcaac catgggatgg ctggaaac tgcttgactt gatgtgtt 660
 gaattccacg ttagcggtt aatgcgttag agatgtggag gaataccgt ggcgaaggcg 720
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 acaccgcccc tcacaccacg agagtcggca acaccgaag tcggtgaggt aaccctgtg 1440
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<210> 113
 <211> 1497
 <212> DNA
 <213> *Alicyclobacillus cycloheptanicus*

<400> 113

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<212> DNA
<213> *Alicyclobacillus cycloheptanicus*

<400> 114

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<211> 770
<212> DNA
<213> *Alicyclobacillus acidoterrestris*

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<223> a, c, g, or t

<220>
<221> modified_base
<222> (770)..(770)
<223> a, c, g, or t

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<213> <i>Alicyclobacillus acidoterrestris</i>	
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nnnnnnnnnn ncnnnnggn nnnncntnn nnnnngnnn nnnnnnnnn nntntcnngg 180

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tnngagtgag ntgataccgc tcgcngcagc cgaacgaccc agcgcagcga gtcagtgagc	360
gaggaagcgg aagagcgcnc aatacgaaa ccgcctctcc ccgcgcgttg gccgattcat	420
taatgcagct ggcacgacag gttcccgac tggaaagcgg gcagtgagcg caacgcaatt	480
aatgtgagtt agctcactca ttaggcaccc caggcttac actttatgct tccggctcgt	540
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tacgccaagc ttggtaccga gctcgatcc actagtaacg gccgccagtg tgctgaaatt	660
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gttctggcc gcacgcgcgc tacactgaca gggccagcgg gtacatcacc ttggccgaga	900
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 majority sequence

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tacgatgtgg acaacacgcg tgatttgcgg aatcgattc cgaaaaatgg cttcggcgaa	420
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cggccggatg ggtgctggtt tggtcgtgg ggcgtcaact acgtgtatgg catgggcgcg	600
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ctcgactggg tcgtggagca tcagaatgcg gatggcggct ggggtgaaga ctgcgcntcn	720
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tacctnnnng anacgcagcg cgcngatggt ggctgnnn	878